21. ~~99~~. (New) The method of claim ~~98~~ 20, wherein the sample comprises mRNA molecules.

22. ~~100~~. (New) A kit for use in the method of claim ~~98~~ 20, wherein said kit comprises at least one nucleic acid probe of claim ~~98~~ 20 and instructions for use in the method of claim ~~98~~ 20.

23. ~~101~~. (New) A method for producing a polypeptide, said method comprising culturing a host cell containing a nucleic acid molecule of claim ~~87~~ 1 under conditions in which the polypeptide encoded by the nucleic acid molecule is expressed.

C 49 cont'd

24. ~~102~~. (New) A method for producing a polypeptide, said method comprising culturing a host cell containing a nucleic acid molecule of claim ~~88~~ 10 under conditions in which the polypeptide encoded by the nucleic acid molecule is expressed.

25. ~~103~~. (New) A method for producing a polypeptide, said method comprising culturing a host cell containing a nucleic acid molecule of claim ~~90~~ 12 under conditions in which the polypeptide encoded by the nucleic acid molecule is expressed.

26. ~~104~~. (New) A method for producing a polypeptide, said method comprising culturing a host cell containing a nucleic acid molecule of claim ~~91~~ 13 under conditions in which the polypeptide encoded by the nucleic acid molecule is expressed.

REMARKS

Status of the Claims:

Claims 63-67, 77-79, and 87-104 are pending in the current application. Claims 61, 62, 68-71, 74-76, and 80-86 have been cancelled without prejudice. New claims 87-104 have been added. Support for the new claims can be found in original claims 3-8, 15, 17, and 18, as well in

the specification on page 59, lines 28-29 and page 62, line 16. No new matter has been added by way of amendment.

Applicant affirms the election of Groups VI and XIX, which have been rejoined by the Examiner, and expressly reserve the right to file divisional applications or take such other appropriate measures deemed necessary to protect the inventions in the remaining claims. Reexamination and reconsideration of the claims are respectfully requested.

In accordance with the Examiner's request, a clean copy of all pending claims has been provided herewith as **Appendix A.**

The Rejection Under 35 U.S.C. §101 Should be Withdrawn:

Claims 61-67, 72-73, and 77-79 have been rejected under 35 U.S.C. § 101 on the grounds that the claimed invention lacks patentable utility. This rejection is respectfully traversed as applied to these claims as well as to new claims 87-104 for the reasons described below.

In rejecting the claims for lack of utility, the Examiner argues that the Applicant has failed to demonstrate, either by sequence comparisons or working examples, that 21612 encodes a dehydrogenase as asserted in the specification. However, analysis of the 21612 sequence indicates that 21612 is a member of the short chain-dehydrogenase family of proteins. The 21612 polypeptide has been compared to the Pfam database of protein families and been shown to share a high degree of sequence similarity with a consensus alignment for short chain dehydrogenases (PFAM Accession No. PF00106). A copy of the alignment of 21612 with the Pfam short chain dehydrogenase consensus sequence is attached as **Appendix B**.

The Pfam database provides a curated collection of well-characterized protein family domains with high quality alignments. Functional domains of novel proteins may be identified by comparison with the Pfam protein family domain alignments. It is well known in the art that regions of sequence homology with consensus domains characteristic of a family of proteins having a know function may be used to determine the function of a novel polypeptide. The sequences included in the Pfam seed alignment used to create the short chain dehydrogenase consensus include proteins that have been well-characterized biochemically; for example an

alcohol dehydrogenase from *Drosophila* (NCBI Accession No. P21898), several human estradiol 17 β-dehydrogenases (NCBI Accession Nos. P37059, P51659, and P14061), a human corticosteroid 11-β-dehydrogenase (NCBI Accession No. P80365), and a human 15-hydroxyprotaglandin dehydrogenase (NCBI Accession No. Accordingly, the fact that the 21612 polypeptide gives a high score when aligned with the Pfam short chain dehydrogenase consensus indicates that 21612 functions as a short chain dehydrogenase.

The United States Patent and Trademark Office "Utility Examination Guidelines" (66 Fed Reg. 1092 (2001)) make it clear that sequence homology is sufficient to establish utility, and that working examples or biochemical evidence are not a *per se* requirement for the establishment of utility. The "Utility Examination Guidelines" state, "[w]hen a patent application claiming a nucleic acid asserts a specific, substantial, and credible utility, and bases the assertion upon homology to existing nucleic acids or proteins having an accepted utility, the asserted utility must be accepted by the examiner unless the Office has sufficient evidence or sound scientific reasoning to rebut such an assertion." (66 Fed. Reg. 1096). Accordingly, the rejection under 35 U.S.C. § 101 has been overcome

In view of the above arguments, all grounds for rejection under 35 U.S.C. §101 have been overcome. Reconsideration and withdrawal of the rejection are respectfully requested.

The Rejections Under 35 U.S.C. §112, First Paragraph, Should be Withdrawn

Claims 61-67, 72-73, and 77-79 have been rejected under 35 U.S.C. § 112, first paragraph on the grounds that the claimed invention lacks utility and therefore one skilled in the art would not know how to use it. The rejection is traversed as applied to these claims as well as to new claims 87-104. As discussed above, the claimed invention does have a specific, substantial, and credible utility, thereby overcoming the grounds of the rejection.

Claims 61-67, 72-73, and 77-79 have been rejected under 35 U.S.C. §112, first paragraph, on the grounds that the specification does not provide enablement for variants of 21612. The rejection is respectfully traversed as applied to these claims, as well as new claims 88-91, 93-97, and 103-104.

The Examiner states that Applicant has not provided guidance sufficient to allow one of skill in the art to make and use nucleotide sequences having a given level of sequence identity with SEQ ID NO:8 because "the relationship between the sequence of a polypeptide and its tertiary sequence is neither well understood nor predictable." August 17, 2001 Office Action page 5. The Examiner also states, "[t]he mere identification of critical regions would not be sufficient, as the ordinary artisan would immediately recognize that the encoded polypeptide must assume the proper three-dimensional configuration to be active." *Id.*, at page 5. As an initial matter, Applicant notes that the rejected claims are not directed to nucleotide sequences encoding a polypeptide having any particular three-dimensional confirmation, but instead are directed to nucleotide sequences having a given level of sequence identity with SEQ ID NO:8, and to nucleotide sequences hybridizing with SEQ ID NO:8 under stringent conditions. While Applicant agrees that some regions of a protein must retain a certain conformation in order for the protein to be active, it does not follow that a protein's tertiary structure must be known in order to determine the activity of that protein. In fact, three-dimensional structures have been elucidated for only a very few of the thousands of proteins having known biochemical or physiological activity.

New claims 88-91 recite nucleotide sequences encoding a polypeptide having dehydrogenase activity, wherein the nucleotide sequence has a designated level of sequence identity with SEQ ID NO:8. New claim 92 recites nucleotide sequences encoding fragments of 21612, wherein the fragments have dehydrogenase activity and comprise at least 139 contiguous amino acids of 21612. Sufficient guidance for making and using the claimed sequences is given in the specification. Applicant has provided the entire 21612 amino acid sequence, SEQ ID NO:7, as well as a nucleotide sequence which encodes it, SEQ ID NO:8 The nucleotide

sequences of claims 88-91 vary from the nucleotide sequence of SEQ ID NO 8 by structural parameters (i.e. percent sequence identity to SEQ ID NO:8, hybridization with the complement of SEQ ID NO:8 under stringent conditions, or deletion) that are defined in the specification, and the claimed variants retain the dehydrogenase activity of the 21612 polypeptide having the amino acid sequence set forth in SEQ ID NO:7. Guidance for determining percent sequence identity and hybridization under stringent conditions is provided in the specification (see page 18, line 4 *et seq.* and page 60, line 8 *et seq.*). Polypeptide sequence variants that retain function are also described in the specification as containing "only conservative variation or variation in non-critical residues or in non-critical regions" (page 21, lines 20-21 of the specification). Guidance regarding conservative substitutions of amino acids is found in the specification on page 17, lines 6-12 and Table 1.

Further, 21612 shares a high level of sequence identity with a consensus domain that is conserved among members of the short chain dehydrogenase family (see **Appendix B**). The specification also teaches methods for determining additional residues that are essential for function, including site-directed mutagenesis and alanine-scanning mutagenesis (page 22, lines 1-10).

Finally, the specification provides guidance regarding assays for dehydrogenase activity on page 22, lines 11-19. Accordingly, one of skill in the art would be able to determine the functionality of 21612 variants.

Thus, a rational scheme for determining the regions of the 21612 short chain dehydrogenase that would tolerate modification is provided. Based on the regions of the 21612 polypeptide that are conserved with other short chain dehydrogenases, and the methods provided for identifying additional residues critical for 21612 function, the skilled artisan could choose among possible modifications to produce polypeptides encodes by nucleotide sequences within structural parameters set forth in the claims and then test these modified variants to determine if they retain dehydrogenase activity. Although some quantity of experimentation would be required, the level of experimentation would not be undue in view of the amount of direction provided in the specification, the state of the prior art, and the level of skill of one of ordinary

skill in the art. These factors all favor a conclusion that one of skill in the art could practice the claimed invention without undue experimentation. Accordingly, the rejection under 35 U.S.C. § 112, first paragraph, has been overcome.

Claims 65 and 66 have been rejected under 35 U.S.C. § 112, first paragraph on the grounds that the specification does not enable host cells that encompass the recited nucleic acid molecules where those host cells are *in vivo*. The rejection is traversed as applied to the rejected claim as well as to new claims 95 and 96 for the reasons described below.

The Examiner argues that because the rejected claims read on host cells *in vivo*, they encompass host cells obtained by gene therapy and host cells present in a transgenic animal, and that methods of gene therapy and methods of producing transgenic animals are unpredictable. Applicant agrees that numerous factors can affect the success of methods of introducing a heterologous gene into a cell *in vivo* by gene therapy or methods of obtaining a transgenic animal. However, vectors and methods for gene therapy and for the production of transgenic animals are well known to those of skill in the art and many factors that determine the success of the methods have been identified. Further, the rejected claims are directed only to those host cells that contain the recited nucleic acid molecules and thus do not read on inoperative embodiments. Accordingly, the enablement of the specification is commensurate with the scope of the claims and the rejection under 35 U.S.C. § 112, first paragraph, has been overcome.

The claims have also been rejected under 35 U.S.C. § 112, first paragraph, on the grounds that the Applicant has not provided the required assurance that all of the conditions for a biological deposit under 37 C.F.R. §1.801-1.809 have been met. A Declaration under 37 C.F.R. §1.802 accompanies the present response, thereby obviating the rejection.

Claims 61 and 72 have been rejected under 35 U.S.C. § 112, first paragraph, on the grounds that Applicant have not provided sufficient written description for the variants and

fragments of 21612 recited in these claims. The rejection is respectfully traversed as applied to new claims 88-92 for the reasons described below.

Claims 88-92 meet the written description guidelines set forth in the "Guidelines for Examination of Patent Applications Under the 35 U.S.C. §112, ¶ 1, 'Written Description' Requirement" (66 Fed. Reg. 1099 (2001)). The guidelines state:

> The written description requirement for a claimed genus may be satisfied through sufficient description of a representative number of species by actual reduction to practice..., reduction to drawings...., or by disclosure of relevant identifying characteristics, *i.e.*, structure or other physical and/or chemical properties, by functional characteristics coupled with a known or disclosed correlation between structure and function, or by a combination of such identifying characteristics, sufficient to show the applicant was in possession of the claimed genus."

66 Fed. Reg. 1106. In the present case, the nucleotide sequences recited in claims 88-92 have been described by both their structural properties (*i.e.* as having a given percent sequence identity with the nucleotide sequence set forth in SEQ ID NO:8, hybridizing to the nucleotide sequence set forth in SEQ ID NO:8 under stringent conditions, or encoding fragments of the amino acid sequence shown in SEQ ID NO:7) and functional characteristics (*i.e.* dehydrogenase activity), thereby meeting the standards set forth in the guidelines. The present claims are comparable to the claim presented in Example 14 of the "Synopsis of Application of Written Description Guidelines" cited in the written description guidelines (66 Fed. Reg. 1101), in which the claimed protein is described by its sequence identity with a second protein and by its function. In the analysis of this example in the Synopsis, it is concluded that the claimed polypeptide is adequately described. Similarly, in the present case the criteria for written description have been met as the nucleotide sequence is defined by structure and function and the rejection should not be applied to claims 88-92.

In view of the above arguments and amendments, all grounds for rejection under 35 U.S.C. § 112, first paragraph have been obviated or overcome. Reconsideration and withdrawal of the rejection is respectfully requested.

The Rejections Under 35 U.S.C. §112, Second Paragraph, Should be Withdrawn

Claims 61, 62, 72, and 79 have been rejected under 35 U.S.C. § 112, second paragraph, for indefiniteness. Claims 61, 62, and 72 have been cancelled and claim 79 has been amended to clarify what is intended by the recited "compound." Accordingly, all grounds for rejection under 35 U.S.C. § 112, second paragraph, have been obviated or overcome and reconsideration and withdrawal of the rejection is respectfully requested.

The Rejection Under 35 U.S.C. § 102(b) Should be Withdrawn

Claims 61, 77, and 78 have been rejected under 35 U.S.C. § 102(b) on the grounds that they are anticipated by the sequence of GenBank Accession No. AA622988. The rejection is traversed as applied to the new and amended claims.

The cited sequence contains a region of 324 nucleotide that are 100% identical to nucleotides 1694 to 2018 of SEQ ID NO:8. New claim 92 encompasses nucleotide sequences encoding fragments of 21612 wherein the fragments comprise 139 contiguous amino acids of the amino acid sequence of SEQ ID NO:7 or 139 contiguous amino acids of the amino acid sequence encoded by the cDNA insert of the plasmid deposited with ATCC as Patent Deposit No. PTA-2170. Support for the new claim can be found on page 62, line 16 of the specification. Accordingly, the cited sequence does not anticipate new claim 92.

New claim 91 encompasses nucleotide sequences encoding a polypeptide having dehydrogenase activity, wherein said sequences hybridize to the complement SEQ ID NO:8 under stringent conditions. Claim 77 has been amended to recite specific nucleic acid probes to be used in the claimed method of detection. Accordingly, claims 77 and 91 are not anticipated by GenBank Accession No. AA622988.

In view of the above amendments, all grounds for rejection under 35 U.S.C. § 102(b) have been overcome. Reconsideration and withdrawal or the rejection is respectfully requested.

CONCLUSIONS

It is believe that all the rejections have been obviated or overcome and the claims are in condition for allowance. Early notice to this effect is solicited.

It is not believed that extensions of time or fees for net addition of claims are required, beyond those that may otherwise be provided for in documents accompanying this paper. However, in the event that additional extensions of time are necessary to allow consideration of this paper, such extensions are hereby petitioned under 37 CFR § 1.136(a), and any fee required therefore (including fees for net addition of claims) is hereby authorized to be charged to Deposit Account No. 16-0605.

Respectfully submitted,

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CERTIFICATE OF MAILING

I hereby certify that this correspondence is being deposited with the United States Postal Service with sufficient postage as first class mail in an envelope addressed to: Commissioner for Patents, Washington, DC 20231, on November 19, 2001.

Nora C. Martinez

Nora C. Martinez

Version with Markings to Show Changes Made:

In the Claims:

Please amend claims 63-65, 67, and 77-79 as follows:

63. (Amended) The nucleic acid molecule of claim 87[61] further comprising vector nucleic acid sequences.

64. (Amended) The nucleic acid molecule of claim 87[61] further comprising nucleic acid sequences encoding a heterologous polypeptide.

65. (Amended) A host cell which contains the nucleic acid molecule of claim 87[61].

67. (Amended) A nonhuman mammalian host cell containing the nucleic acid molecule of claim 87[61].

77. (Amended) A method for detecting the presence of a nucleic acid molecule of claim 87[61] in a sample, said method comprising the steps of[:

a)]contacting the sample with a nucleic acid probe [or primer] which selectively hybridizes to the nucleic acid molecule[;] and

[b)]determining whether the nucleic acid probe or primer binds to a nucleic acid molecule in the sample; wherein said nucleic acid probe is selected from the group consisting of

a) the nucleotide sequence set forth in SEQ ID NO:8;

b) the nucleotide sequence of a fragment of the nucleotide sequence set for in SEQ ID NO:8, wherein said fragment comprises at least 417 contiguous nucleotides of the nucleotide sequence set forth in SEQ ID NO:8;

c) a nucleotide sequence having at least 70% sequence identity to the nucleotide sequence set forth in SEQ ID NO:8; and

d) a nucleotide sequence complementary to a nucleotide sequence of a), b), or c).

78. (Amended) The method of claim 77, wherein the sample comprises mRNA molecules [and is contacted with a nucleic acid probe].

79. (Amended) A kit for use in the method of claim 77, wherein said kit comprises at least one nucleic acid probe of claim 77[comprising a compound which selectively hybridizes to a nucleic acid molecule of claim 61] and instructions for use in the method of claim 77.

In re: Meyers
Appl. No. 09/464,039
Filed December 15, 1999

OIPE JC29
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APPENDIX A

OIPE JC29
JAN 15 2002
PATENT & TRADEMARK OFFICE

Claims Pending after Amendment of November 19, 2001

63. (Amended) The nucleic acid molecule of claim 87 further comprising vector nucleic acid sequences.

64. (Amended) The nucleic acid molecule of claim 87 further comprising nucleic acid sequences encoding a heterologous polypeptide.

65. (Amended) A host cell which contains the nucleic acid molecule of claim 87.

66. The host cell of claim 65 which is a mammalian host cell.

67. (Amended) A nonhuman mammalian host cell containing the nucleic acid molecule of claim 87.

77. (Amended) A method for detecting the presence of a nucleic acid molecule of claim 87 in a sample, said method comprising the steps of contacting the sample with a nucleic acid probe which selectively hybridizes to the nucleic acid molecule and determining whether the nucleic acid probe binds to the nucleic acid molecule in the sample; wherein said nucleic acid probe is selected from the group consisting of:

a) the nucleotide sequence set forth in SEQ ID NO:8;

b) the nucleotide sequence of a fragment of the nucleotide sequence set for in SEQ ID NO:8, wherein said fragment comprises at least 417 contiguous nucleotides of the nucleotide sequence set forth in SEQ ID NO:8;

c) a nucleotide sequence having at least 70% sequence identity to the nucleotide sequence set forth in SEQ ID NO:8; and

d) a nucleotide sequence complementary to a nucleotide sequence of a), b), or c).

78. (Amended) The method of claim 77, wherein the sample comprises mRNA molecules.

79. (Amended) A kit for use in the method of claim 77, wherein said kit comprises at least one nucleic acid probe of claim 77 and instructions for use in the method of claim 77.

87. (New) An isolated nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of:

a) the nucleotide sequence set forth in SEQ ID NO:8;

b) the nucleotide sequence of the cDNA insert of the plasmid deposited with ATCC as Patent Deposit Number PTA-2170;

c) a nucleotide sequence encoding the amino acid sequence set forth in SEQ ID NO:7;

d) a nucleotide sequence encoding the amino acid sequence encoded by the cDNA insert of the plasmid deposited with ATCC as Patent Deposit Number PTA-2170; and

e) a nucleotide sequence complementary to a nucleotide sequence of a), b), c), or d).

88. (New) An isolated nucleic acid molecule having a nucleotide selected from the group consisting of:

a) a nucleotide sequence encoding a polypeptide having dehydrogenase activity, wherein said nucleotide sequence has at least 70% sequence identity with the nucleotide sequence set forth in SEQ ID NO:8; and

b) a nucleotide sequence complementary to the nucleotide sequence of a).

89. (New) The nucleic acid molecule of claim 88, wherein said nucleotide sequence is selected from the group consisting of:

a) a nucleotide sequence encoding a polypeptide having dehydrogenase activity, wherein said nucleotide sequence has at least 80% sequence identity with the nucleotide sequence set forth in SEQ ID NO:8; and

b) a nucleotide sequence complementary to the nucleotide sequence of a).

90. (New) The nucleic acid molecule of claim 89, wherein said nucleotide sequence is selected from the group consisting of:

a) a nucleotide sequence encoding a polypeptide having dehydrogenase activity, wherein said nucleotide sequence has at least 90% sequence identity with the nucleotide sequence set forth in SEQ ID NO:8; and

b) a nucleotide sequence complementary to the nucleotide sequence of a).

91. (New) An isolated nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of:

a) a nucleotide sequence encoding a polypeptide having dehydrogenase activity, wherein the complement of said nucleotide sequence hybridizes under stringent conditions to the nucleotide sequence set forth in SEQ ID NO:8, said stringent conditions comprising hybridization at about 45°C, followed by at least one wash in 0.2X SSC/0.1% SDS at 65°C; and

b) a nucleotide sequence complementary to the nucleotide sequence of a).

92. (New) An isolated nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of

a) a nucleotide sequence encoding a fragment of the amino acid sequence set forth in SEQ ID NO:7, wherein said fragment has dehydrogenase activity and consists of at least 139 contiguous amino acids of SEQ ID NO:7; and

b) a nucleotide sequence encoding a fragment of the amino acid sequence encoded by the cDNA insert of the plasmid deposited with ATCC as Patent Deposit Number PTA-2170, wherein the fragment has dehydrogenase activity and consists of at least 139 contiguous amino acids of the amino acid sequence encoded by the cDNA insert of the plasmid deposited with ATCC as Patent Deposit Number PTA-2170; and

c) a nucleotide sequence complementary to the nucleotide sequence of a) or b).

93. (New) The nucleic acid molecule of claim 88 further comprising vector nucleic acid sequences.

94. (New) The nucleic acid molecule of claim 88 further comprising nucleic acid sequences encoding a heterologous polypeptide.

95. (New) A host cell which contains the nucleic acid molecule of claim 88.

96 (New) The host cell of claim 95, wherein said host cell is a mammalian host cell.

97. (New) A nonhuman mammalian host cell containing the nucleic acid molecule of claim 88.

98. (New) A method for detecting the presence of a nucleic acid molecule of claim 88 in a sample, said method comprising the steps of contacting the sample with a nucleic acid probe which selectively hybridizes to the nucleic acid molecule and determining whether the nucleic acid probe or primer binds to a nucleic acid molecule in the sample; wherein said nucleic acid probe is selected from the group consisting of:

a) the nucleotide sequence set forth in SEQ ID NO:8;

b) the nucleotide sequence of a fragment of the nucleotide sequence set for in SEQ ID NO:8, wherein said fragment comprises at least 417 contiguous nucleotides of the nucleotide sequence set forth in SEQ ID NO:8;

c) a nucleotide sequence having at least 70% sequence identity to the nucleotide sequence set forth in SEQ ID NO:8; and

d) a nucleotide sequence complementary to a nucleotide sequence of a), b), or c).

99. (New) The method of claim 98, wherein the sample comprises mRNA molecules.

100. (New) A kit for use in the method of claim 98, wherein said kit comprises at least one nucleic acid probe of claim 98 and instructions for use in the method of claim 98.

101. (New) A method for producing a polypeptide, said method comprising culturing a host cell containing a nucleic acid molecule of claim 87 under conditions in which the polypeptide encoded by the nucleic acid molecule is expressed.

102. (New) A method for producing a polypeptide, said method comprising culturing a host cell containing a nucleic acid molecule of claim 88 under conditions in which the polypeptide encoded by the nucleic acid molecule is expressed.

103. (New) A method for producing a polypeptide, said method comprising culturing a host cell containing a nucleic acid molecule of claim 90 under conditions in which the polypeptide encoded by the nucleic acid molecule is expressed.

104. (New) A method for producing a polypeptide, said method comprising culturing a host cell containing a nucleic acid molecule of claim 91 under conditions in which the polypeptide encoded by the nucleic acid molecule is expressed.

Protein Family / Domain Matches, HMMer version 2

```
Searching for complete domains
hmmpfam - search a single seq against HMM database
HMMER 2.1.1 (Dec 1998)
Copyright (C) 1992-1998 Washington University School of Medicine
HMMER is freely distributed under the GNU General Public License (GPL).
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
HMM file:                 /prod/ddm/seqanal/PFAM/pfam4.3/Pfam
Sequence file:            /prod/ddm/wspace/orfanal/oa-script.6378.seq
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
 Query:  21612

Scores for sequence family classification (score includes all domains):
Model          Description                                   Score    E-value  N
--------       -----------                                   -----    ------- ---
adh_short       short chain dehydrogenase                    145.0    1.3e-39   1
beta-lactamase  Beta-lactamase                                 3.3        6.6   1

Parsed for domains:
Model          Domain  seq-f seq-t    hmm-f hmm-t       score  E-value
--------       ------- ----- -----    ----- -----       -----  -------
adh_short        1/1      11   204 ..     1   203 []    145.0  1.3e-39
beta-lactamase   1/1     222   236 ..   317   331 .]      3.3      6.6

Alignments of top-scoring domains:
adh_short: domain 1 of 1, from 11 to 204: score 145.0, E = 1.3e-39
                   *->KvaLvTGassGIGlaiAkrLakeGakVvvadrneeklekG.....av
                       ++ +TGas+GIG+aiA+  ak+Ga++v+a+ ++ +  k+ ++    +
       21612    11    CTVFITGASRGIGKAIALKAAKDGANIVIAAKTAQPHPKLlgtiyTA 57

                   akelkelGgndkdralaiqlDvtdeesv.aaveqaverlGrlDvLVNNAG
                   a+e+++ Gg     +al++ +Dv+de++++aave+a++++G++D+LVNNA
       21612    58 AEEIEAVGG----KALPCIVDVRDEQQIsAAVEKAIKKFGGIDILVNNAS 103

                   giillrpgpfaelsrtmeedwdrvidvNltgvflltravlplmamkkrgg
                      ++  ++ ++ +     +  d +++vN +g+ l ++a++p   +kk++
       21612   104 ---AISLTNTLDTP---TKRLDLMMNVNTRGTYLASKACIP--YLKKSKV 145

                   GrIvNiSSvaGrkeg.glvgvpgg..saYsASKaAvigltrsLAlElaph
                     I NiS       +  l++v++ +++aY+ +K ++ +    ++A E +
       21612   146 AHILNISP------PlNLNPVWFKqhCAYTIAKYGMSMYVLGMAEEFKGE 189

                   gIrVnavaP.GgvdTd<-*
                    I Vna  P+ ++ T+
       21612   190 -IAVNALWPkTAIHTA    204

beta-lactamase: domain 1 of 1, from 222 to 236: score 3.3, E = 6.6
                   *->eliaeaakvvleaLg<-*
                      ++ia+aa++++++ +
       21612   222    DIIADAAYSIFQKPK    236

//
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APPENDIX B